



Figure 16: Multiple Sequence Alignments of Mil.1, Mil.2 and Rpi-blb2 nucleic acids

CLUSTAL W (1.82) Multiple Sequence Alignments

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Sequence format is Pearson
Sequence 1: Mil.1          3768 bp
Sequence 2: Mil.2          3774 bp
Sequence 3: Rpi-blb2       3804 bp
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 95
Sequences (1:3) Aligned. Score: 89
Sequences (2:3) Aligned. Score: 89
Guide tree file created: [/ebi/extern/cluster-work/interactive/clusterw-
20040503-14435620.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2      Score:68908
Group 2: Sequences: 3      Score:65855
Alignment Score 66872
CLUSTAL-Alignment file created [/ebi/extern/clusterw-work/interactive/clusterw-
20040503-14435620.aln]
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CLUSTAL W (1.82) multiple sequence alignment

Mil.1	ATGGAACAAACGAAAGATAATGAAGAAAGCAAACTCATTTGGTGCTATTTCTGCTCTT	60
Mil.2	ATGGAACAAACGAAAGATAATGAAGAAAGCAAACTCATTTGGTGCTATTTCTGCTCTT	60
Rpi-blb2	ATGGAACAAACGAAAGATAATGAAGAAAGCAAACTCATTTGGTGCTATTTCTGCTCTT	60
*****		*****

Mi1.1	AGCAAGGACATGCCGATGTTCTGGTTTTCCTAGAGA-----ATGAGGAAAATCAA	111
Mi1.2	AGCAAGGACATTGCCAATGTTCTAAATTTTCCTAGAGA-----ATGAGGAAAATCAA	111
Rpi-blb2	CGCAAGGATGCTGCCAATGTTCTGGATTTTCCTAGAGAGATTAAAGAATGAAAGAATCAA	120
	*****	*****
Mi1.1	AAAGCTCTTGACAAAGATCAAGTTGAAAAGATAAAAATTGAAAATGGCATTATTGTACA	171
Mi1.2	AAAGCTCTTGACAAAGATCAAGTTGAAAAGCTAAAAATTGAAAATGGCATTATTGTACA	171
Rpi-blb2	AAGGCTGTTGATGTGGATCTGATTGAAAGCCTGAAAATTGAAGCTGACATTTATTGTACA	180
	** ***	*****
Mi1.1	TATGTTCAGCTTCTTGTTCGGATTTTGAGCAGTTTGAAAGATATAATGACTAGAAAAAGA	231
Mi1.2	TATGTTCAGCTTCTTATTCCGATTTTGAGCAGTTTGAAAGATATAATGACTAGAAAAAGA	231
Rpi-blb2	TATGTCCAGCTTCTTATTCCGATTTTGGAGAAAGTTTGAAAGATATAATGACTAGAAAAAGA	240
	*****	*****
Mi1.1	CAAGAGGTTGAGAAATCTGCTTCAACCACTTTTGGATGATGATG-----	274
Mi1.2	CAAGAGGTTGAGAAATCTGCTTCAATCACTTTTGGATGATGATG-----	274
Rpi-blb2	CAAGAGGTTGAGAAATCTGCTTCAACCAATTTTGGATGATGATGGCAAAGACGTCGGGTGT	300
	*****	*****
Mi1.1	-----TCTTTACTAGCCTCACCAGTAATAATGGATGACTGTATCAGCTTGTATCATCGT	327
Mi1.2	-----TCCTTACTAGCCTCACCAGTAATAATGGATGACTGTATCAGCTTGTATCATCGT	327
Rpi-blb2	AAATATGTCCTTACTAGCCTCGCCGGTAATAATGGATGACTGTATAAGCTTGTATCATCGT	360
	** *****	*****
Mi1.1	TCTTATAAATCAGATGCCATCATGATGGATGAGCAATTGGACTTCCTCCTTGAATCTC	387
Mi1.2	TCTTATAAATCAGATGCCATCATGATGGATGAGCAATTGGACTTCCTCCTTGAATCTG	387
Rpi-blb2	TCT---AAATCAGATGCCACCATGATGGATGAGCAATTGGGCTTCCTCCTTGAATCTC	417
	*** *****	*****

Mi1.1	TATCATCTATCCAAGCATCACGCTGAAAGATATTTCTCTGGAGTGACTCAATATGAAGTT	447
Mi1.2	TATCATCTATCCAAGCATCACGCTGAAAGATATTTCTCTGGAGTGACTCAATATGAAGTT	447
Rpi-blb2	TCTCATCTATCCAAGCATCGTGTGAAAGATGTTTCTCTGGAGTGACTCAATATGAAGTT	477
	* ****	***
Mi1.1	CTTCAGAAATATATGTGGCAACATAAGAGATTTCCATGGGTTGATAGTGAATGGTTGCATT	507
Mi1.2	CTTCAGAAATGTATGTGGCAACATAAGAGATTTCCATGGGTTGATAGTGAATGGTTGCATT	507
Rpi-blb2	CTTCAGAAATGTATGTGGCAACATAAGAGATTTCCATGGATTTGATAGTGAATGTTTGCATT	537
	*****	*****
Mi1.1	AAGCATGAGATGGTTGAGAATGTCTTRCCTCTGTCTTCAACTCATGGCTGACAGAGTAGGA	567
Mi1.2	AAGCATGAGATGGTTGAGAATGTCTTACCTCTGTCTTCAACTCATGGCTGAAAGAGTAGGA	567
Rpi-blb2	AAGCATGAGATGGTTGAGAATGTCTTATCTCTGTCTTCAACTGATGGCTGAGAGAGTAGGA	597
	*****	*****
Mi1.1	CAC TTCCTTTGGGATGATCAGACTGATGAAGACTCTCGACTCTCCGAGCTAGATGAGGAT	627
Mi1.2	CAC TTCCTTTGGGAGGATCAGACTGATGAAGACTCTCGGCTCTCCGAGCTAGATGAGGAT	627
Rpi-blb2	CGCTTCCTTTGGGAGGATCAGGCTGATGAAGACTCTCAACTCTCCGAGCTAGATGAGGAT	657
	* ****	*****
Mi1.1	GAACAAAATGATAGAGACTCTCGACTTTTCAAGCTAGCACATCTACTCTTGAAGATCGTT	687
Mi1.2	GAACACAAATGATAGAGACTCTCGACTCTTCCAGCTAACACATCTACTCTTGAAGATTGTT	687
Rpi-blb2	GATCAGAAATGATAAAGACCCCTCAACTCTTCAAGCTAGCACATCTACTCTTGAAGATTGTT	717
	** **	***
Mi1.1	CCGGTTGAACTGGAGGTTATACACATATGTTATACAAACTTGAAAGCTTCAACTTCAGCT	747
Mi1.2	CCAACTGAACTGGAGGTTATGCACATATGTTATACAAATTTGAAAGCTTCAACTTCAGCA	747
Rpi-blb2	CCAACTGAAATGGAGGTTATGCACATATGTTATAAAACTTTGAAAGCTTCAACTTCAACA	777
	** ****	*****
Mi1.1	GAAGTTGGACTCTTTCATTAAGCAGCTTCTAGAAACCCTCTCCAGATATTTCTGAGGGAATAT	807

Mi1.2	GAAGTTGGACGCTTCATTAAGAAGCTCCTGGAAACCTCACCGGATATTCTCAGAGAATAT	807
Rpi-blb2	GAAATTGGACGCTTCATTAAGAAGCTCCTGGAAACCTCTCCGGACATTCTCAGAGAATAT	837
	*** ***** ***** ** ** ***** ** ** ***** ** *****	
Mi1.1	CTAATTCTCTGCAAGAGCACATGGTAACGTGTTATTACCCCTAGCACCTCAGGGGCTCGA	867
Mi1.2	ATCATTTCAACTACAAGAGCATATGTTAACTGTTATTCCCCCTAGCACCTTAGGGGCTCGA	867
Rpi-blb2	CTGATTTCATCTACAAGAGCATATGATAACTGTTATTACCCCTAACACACTTCAGGGGCTCGA	897
	* *** ** ***** ** ** ***** ***** ***** *****	
Mi1.1	AACATTTCATGTCATGATGGAAATTCCTATTACTTATTCTTTCTGTATATGCC--CAAGGAC	924
Mi1.2	AACATTTCATGTCATGATGGAAATTCCTATTACTTATTCTTTCTGTATATGCC--CAAGGAC	924
Rpi-blb2	AACATTTCATGTCATGATGGAAATTCCTATTGATTTATTCTTTCTGTATATGCCGCCCAAGGAC	957
	***** ***** ***** ***** ***** ***** *****	
Mi1.1	TTTATTTCATCATGACAAACTTTTGTGATCTCTTGGATCGTGTGCGAGTACTTACCAGGGAG	984
Mi1.2	TTTATTTCATCATGACAAACTTTTGTGATCTCTTGGCTCATGTTGGAACACTTACCAGGGAG	984
Rpi-blb2	TTTATTTCATCATGACAAACTTTTGTGATCTCTTGGCTCGTGTGTAGCACTTACCAGGGAG	1017
	***** ***** ***** ***** ***** ** *** * ***** *****	
Mi1.1	GTATCAACTCTTGTACGTGACTTGGAAAGAGGAACCAAGGAATAAAGAGGGTAATAACCAA	1044
Mi1.2	GTATCGACTCTTGTACGTGACTTGGAAAGAGAAAATTAAGGAATAAAGAGGGTAATAACCAA	1044
Rpi-blb2	GTATCAACTCTTGTACGCGACTTGGAAAGAGAAAATTAAGGATTAAAGAGAGTACTGACGAA	1077
	***** ***** ***** ***** ***** ** ***** ***** ** * **	
Mi1.1	ACAAATTGTGCAACCCCTAGACTTGCTGTGGAATAATTGAACTCCTCAAGAAAGATCTCAA	1104
Mi1.2	ACAAATTGTGCAACCCCTAGACTTGCTGTGGAATAATTGAACTCCTCAAGAAAGATCTCAA	1104
Rpi-blb2	ACAAATTGTGCAACCCCTAAAGTTTCTGGAATAATAATTGAACTCCTTAAGGAAGATCTCAA	1137
	***** ***** ***** * ** ***** ***** ***** *****	
Mi1.1	CATGTTTATCTGAAAGCCCTGGATTCACTCAATGTTGCTTCCCCATGAGTGATGGACCA	1164
Mi1.2	CATGTTTATCTGAAAGCCCAAAATTCATCTCAATGTTGCTTCCCCATGAGTGATGGACCA	1164

Rpi-blb2	CATGTTTATCTGAAAAGTCCCGGATTTCATCTCAATATTGCTTCCCCATGAGTGATGGACCT 1197 ***** ** *****
Mil1.1	CTCTTCATGCATCTTCTACACATACACTTAAATGATTGTGTAGATTCTAATGCTTATTCA 1224
Mil1.2	CTCTTCATGCATCTTCTACACATGCACCTAAATGATTGTGTAGATTCTAATGCTTATTCA 1224
Rpi-blb2	CTCTTCATGCATCTGCTACAGAGACACTTAGATGATTGTGTGGATTCCAATGCTTATTCA 1257 ***** ** *****
Mil1.1	ATTGCTTTGATAAAGGAAGAAATCGAGCTGGTGAAGCAAGACCTGAAATTCATAAGATCA 1284
Mil1.2	ATTTCTTTGATAAAGGAAGAAATCGAGTTGGTGAGTCAAGAACTGGAATTCATAAGATCA 1284
Rpi-blb2	ATTGCTTTGATAAAGGAACAAATTGGGCTGGTGAAAGAAGACTTGGAATTCATAAGATCT 1317 ** ***** ** * *****
Mil1.1	TTCTTTTGTGGATGCTG--AGCAAGGATTGTATAAAGATCTCTGGGCACGTGTTCTAGAT 1341
Mil1.2	TTCTTTGGGATGCTGCTGAGCAAGGATTGTATAAAGATATCTGGGCACGTGTTCTAGAT 1344
Rpi-blb2	TTTTTCGCGAATATTG--AGCAAGGATTGTATAAAGATCTCTGGGAACGTGTTCTAGAT 1374 ** ** * ** ** *****
Mil1.1	GTGGCTTATGAGGCAAAAGATGTCATAGATTCAATTATTGTTTCGAGATAATGGTCTCTTA 1401
Mil1.2	GTGGCTTATGAGGCAAAAGATGTCATAGATTCAATTATTGTTTCGAGATAATGGTCTCTTA 1404
Rpi-blb2	GTGGCATATGAGGCAAAAGATGTCATAGATTCAATTATTGTTTCGAGATAATGGTCTCTTA 1434 ***** *****
Mil1.1	CATCTTATTTTCTCACTTCCCATTACCATAAAGAAGATCAAACTTATCAAAAGAAGAGATC 1461
Mil1.2	CATCTTATTTTCTCACTTCCCATTACCATAAAGAAGATCAAACTTATCAAAAGAAGAGATC 1464
Rpi-blb2	CATCTTATTTTCTCACTTCCCATTACCAGAAAGAAGATGATGCTTATCAAAAGAAGAGGTC 1494 ***** *****
Mil1.1	TCTGCTTTAGATGAGAACATTCCCAAGGACAGAGGTCTAATCGTTGTGAACCTCTCCCAAG 1521
Mil1.2	TCTGCTTTAGATGAGAACATTCCCAAGGACAGAGGTCTAATCGTTGTGAACCTCTCCCAAG 1524
Rpi-blb2	TCTGATTTACATGAGAACATTTCCAAGAACAGAGGTCTCATCGTTGTGAACCTCTCCCAAG 1554

Amendment dated October 24, 2007

Reply to Office Action of April 24, 2007

Annotated Sheets Showing Changes

AAACCCAGTTGAGAGAAAGTCATTGACAACTGATAAAATAACTGTAGGTTTGTAGGAGGAA 1581

Mi1.2 AAACCGATTGAGAGAAAGTCATTGACAACTGATAAAATAATTGTAGGTTTTTGAGGAGGAG 1584

Rp1-blb2
AAACCAGTTGAGAGCAAGTCATTGACAACTGATAAAATAATTGTAGGTTTTGGTGAGGAG 1614

Mi1.1
ACAAACTTGATACTTAGAAAGCTCACCAAGTGGATCGGCAGATCTAGATGTCATTTCGATC 1641

mi1.2
ACAAACTTGATACCTTAGAAAGCTCACCAGTGGACCCGCAGATTTAGATGTCATTTTCGATC 1644

Rpi-blb2
ACAAACTTGATACCTTAGAAAGCTCACCACTGGACCGCAGATCTAGATGTCATTTTCGATC 1674

ACTGGTATGCCGGGTTCAGGTAAACTACTTTGGCATACAAAGTATACAATGATAAGTCA 1701

Mi1.2
ACCGGTATGCCGGGTTCAGGTAAACTACTTTGGCATACAAGTATACAATGATAAGTCA 1704

Rpi-blb2
ATTGGTATGCCGGGTTTAGGTAAACTACTTTGGCGTACAAAGTATACAATGATAAATCA 1734

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Mil.1
GTTTCTAGCCGTTTCGACCTTCGTGCATGGTGCACGGTCACCAAGGATGTGATGAGAAG 1761

Mi1.2
GTTTCTAGACATTTTGACCTTCGTGCATGGTGCACGGTCGATCAAGGATATGACGACAAG 1764

Rp1-blb2 GTTCTAGCCATTTCGACCTTCGTGCATGGTGCA CGGTCGACCAAGTATATGACGAGAAG 1794

[illegible]

Mil.1
 AAGTTGTTGAATACAATTTCAGTCAAGTTAGTGACTCAGATTCAAAATTGAGTGAGAAAT 1821

Mi1.2
AAGTTGTTGGATACAAATTTTCAGTCAAGTTAGTGGCTCAGATTCAAATTTTGAGTGAGCAAT 1824

Rpi-blb2
AAGTTGTTGGATAAAATTTTCAATCAAGTTAGTGACTCAAAATTCAAAAATTGAGTGAGAAT 1854

[illegible]

Mil.1
 ATTGATGTTGCTGATAAATTACGGAAACAACCTGTTTGGAAAGAGGTATCTTATTGTCTTA 1881

mi1.2
ATTGATGTTGCTGATAAAATTGCGGAAACAAC TGT TTGGAAGAGGTATCTTATTGTCTTA 1884

Rp1-blb2
ATTGATGTTGCTGATAAACTACGGAAA CAATTGTTTGGAAGAGGTATCTTATTGTCTTA 1914

Mi1.1	GATGACGTGTGGGATACTACTACATGGGATGAGTTAAACAAGACCTTTTCCTGAATCTAAG	1941
Mi1.2	GATGATGTGTGGGATACTACTACTACATTTGGATGAGTTGACAAGACCTTTTCCTGAAGCTAAG	1944
Rpi-blb2	GATGACGTGTGGGATACTAAATAACATGGGATGAGCTAAACAAGACCTTTTCCTGATGGTATG	1974
	*****	*****
	*****	*****
Mi1.1	AAAGGAAGTAGGATTATTTTGACAACCTCGGGAAGGAAGTGCGTTTGCATGGAAAGCTG	2001
Mi1.2	AAAGGAAGTAGGATTATTTTGACAACCTCGAGAAAAGGAAGTGCGTTTGCATGGAAAGCTG	2004
Rpi-blb2	AAAGGAAGTAGAATTATTTTGACAACCTCGAGAAAAGAAAGTTGCTTTGCATGGAAAGCTC	2034
	*****	*****
	*****	*****
Mi1.1	AACACTGATCCTCTTGACCTTCGATTGCTAAGACCAGATGAAAGTTGGGAACCTATTAGAG	2061
Mi1.2	AACACTGATCCTCTTGACCTTCGATTGCTAAGACCAGATGAAAGTTGGGAACCTTTTAGAT	2064
Rpi-blb2	TACACTGATCCTCTTAACCTTCGATTGCTAAGATCAGAAGAAAGTTGGGAGTTATTAGAG	2094
	*****	*****
	*****	*****
Mi1.1	AAAAGGGCATTTGGGAATGAGAGTTGCCCTGATGAACCTATTAGATGTCGGTAAAGAAATA	2121
Mi1.2	AAAAGGACATTTGGTAATGAGAGTTGCCCTGATGAACCTATTAGATGTCGGTAAAGAAATA	2124
Rpi-blb2	AAAAGGGCATTTGGAAACGAGAGTTGCCCTGATGAACCTATTGGATGTTGGTAAAGAAATA	2154
	*****	*****
	*****	*****
Mi1.1	GCCGAAAATTGTAAAGGGCTTCCTTTTGGTGGCTGATCTGATTGCTGGAGTCATTGCTGGG	2181
Mi1.2	GCCGAAAATTGTAAAGGGCTTCCTTTTGGTGGCTGATCTGATTGCTGGAGTCATTGCTGGG	2184
Rpi-blb2	GCCGAAAATTGTAAAGGGCTTCCTTTTGGTGGTGGATCTGATTGCTGGAATCATTGCTGGG	2214
	*****	*****
	*****	*****
Mi1.1	AGGGAAAAGAAAAGGAGTGTGTGGCTTGAAGTTCAAAGTAGTTTGAGTCTTTTATTTTTG	2241
Mi1.2	AGGGAAAAGAAAAGGAGTGTGTGGCTTGAAGTTCAAAGTAGTTTGAGTCTTTTATTTTTG	2244
Rpi-blb2	AGGGAAAAGAAAAGGAGTGTGTGGCTTGAAGTTGTAATAATTGCAATTCCTTTATTTTTG	2274
	*****	*****
	*****	*****

Mi1.1	AACAGTGAAAGTGGAAGTGATGAAAAGTTATAGAATTAAAGTTATGACCAATTACCACATCAC	2301
Mi1.2	AACAGTGAAAGTGGAAGTGATGAAAAGTTATAGAATTAAAGTTATGACCAATTACCACATCAC	2304
Rpi-blb2	AAGAAATGAAAGTGGAAGTGATGAAAAGTTATAGAATAAAGTTATGACCACTTACCCTGATCAC	2334
	** * *****	*****
Mi1.1	CTCAAGCCATGCTTGCTGTATTTTGCAAGTTTTCGGAAGGACACTTCATTGACAATCTAT	2361
Mi1.2	CTCAAGCCATGCTTGCTTACCTTTTGCAAGTTGGCCGAAGGACACTCCTTTGACAATCTAT	2364
Rpi-blb2	CTGAAGCCATGCTTGCTGTACTTTTGCAAGTGCGCCGAAGGACTGGGTAACGACAATCCAT	2394
	** *****	*****
Mi1.1	GAGTTGAATGTTTATTTCGGTGCTGAAGGATTTGTGGGAAAAGACGGAGATGAACAGTATG	2421
Mi1.2	TTGTTTACTGTATTATTGGGTGCTGAAGGATTTGTGGAAAAGACGGAGATGAAGGGTATA	2424
Rpi-blb2	GAGTTGAAACTTATTTGGGGTTTGAAGGATTTGTGGAAAAGACAGATATGAAGAGTCTG	2454
	*** * ** **	*****
Mi1.1	GAAGAAGTGGTGAAGATTTATATGGATGATTTAATTTACAGTAGCTTGGTAAATTTGTTTC	2481
Mi1.2	GAAGAAGTGGTGAAGATTTATATGGATGATTTAATTTCCAGTAGCTTGGTAAATTTGTTTC	2484
Rpi-blb2	GAAGAAGTGGTGAAGATTTATTTGGATGATTTAATTTCCAGTAGCTTGGTAAATTTGTTTC	2514
	*****	*****
Mi1.1	AATGAGATAGGTTATGCACCTGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTGTTG	2541
Mi1.2	AATGAGATAGGTGATATACTGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTGTTG	2544
Rpi-blb2	AATGAGATAGGTGATTAACCTACTTGCCAACTTCATGATCTTGTGCATGACTTTTGTGTTG	2574
	*****	*****
Mi1.1	ATAAAAGCAAGAAAGGAAAAATTTGTTTGATCAGATAAGATCAAGTGCTCCATCAGATTG	2601
Mi1.2	ATAAAAGCAAGAAAGGAAAAATTTGTTTGATCGGATAAGATCAAGTGCTCCATCAGATTG	2604
Rpi-blb2	ATAAAAGCAAGAAAGGAAAAAGTTGTGTGATCGGATAAGTTCAAGTGCTCCATCAGATTG	2634
	*****	*****
Mi1.1	TTGCCCTCGTCAAATTACCATTGATTGTGATGAGGAGGAG - - - CACTTTGGGCTTAATTT	2658

Mi1.2	TTGCCCTCGTCAAATTACCATTTGATTATGATGAGGAGGAGCACCTTTGGGCTTAATTTT	2664
Rpi-blb2	TTGCCACGTCAAATTAGCATTTGATTATGATGATGATGAAGAGCACCTTTGGGCTTAATTTT	2694
	*****	*****
Mi1.1	GTCATGTTTCGATTCAAATAAGAAAAGGCATTCTGGTAAACACCTCTATTCTTTGAGGATA	2718
Mi1.2	GTCATGTTTCGATTCAAATAAGAAAAGGCATTCTGGTAAACACCTCTATTCTTTGAGGATA	2724
Rpi-blb2	GTCCGTGTTTCGGTTCAAATAAGAAAAGGCATTCCGGTAAACACCTCTATTCTTTGACCATA	2754
	***	***
Mi1.1	ATTGGAGACCAGCTGGATGACAGTGTCTTCTGATGCATTTACCTAAGACACTTGAGGCTT	2778
Mi1.2	AATGGAGACCAGCTGGATGACAGTGTCTTCTGATGCATTTACCTAAGACACTTGAGGCTT	2784
Rpi-blb2	AATGGAGATGAGCTGGACGACCATCTTCTGATACATTTTCATCTAAGACACTTGAGGCTT	2814
	* *	*****
Mi1.1	CTTAGAGTGTGGACCTGCATACGTCCTTTTATCATGGTGAAAGATTCTTTGCTGAATGAA	2838
Mi1.2	ATTAGAGTGTGGACCTGGAAACCTCTTTAATCATGGTGAATGATTCTTTGCTGAATGAA	2844
Rpi-blb2	CTTAGAACCTTGCAACCTGGAATCCTCTTTTATCATGGTTAAAGATTCTTTGCTGAATGAA	2874
	*****	*****
Mi1.1	ATATGCATGTTGAATCATTTGAGGTACTTATCCATTGACACACAAGTTAAATATCTGCCT	2898
Mi1.2	ATATGCATGTTGAATCATTTGAGGTACTTAAAGAAATTCGGACACACAAGTTAAATATCTGCCT	2904
Rpi-blb2	ATATGCATGTTGAATCATTTGAGGTACTTAAAGCATTTGGGACAGAAGTTAAATCTCTGCCT	2934
	*****	*****
Mi1.1	TTGTCTTTTCTCAAACCTCTGGAATCTAGAAAAGCCTGTTTGTGTCTACCAACAGATCAATC	2958
Mi1.2	TTCTCTTTTCTCAAACCTCTGGAATCTAGAAAAGTCTGTTTGTGTCTAACAAGGATCAATC	2964
Rpi-blb2	TTGTCTTTTCTCAAACCTCTGGAATCTAGAAAATCTTGTTTGTGGATAACAAGAATCAACC	2994
	**	*****
Mi1.1	TTGGTACTATTACCGAGAAATTTTGGATCTTGTAAAGTTGCGAGTGCTGTCCGTGGATGCT	3018
Mi1.2	TTGGTACTATTACCGAGAAATTTTGGATCTTGTAAAGTTGCGAGTGCTGTCCGTGGTGCT	3024

Rpi-blb2	TTGATACTATTACCGAGAAATTTGGGATCTTGTAAAGTTGCAAGTGCTGTTCACGACTGCT 3054 *** ****
Mil.1	TGTTCTTTCTTTTGATATGGATGCAGATGAATCAATATTGATAGCAGAGGACACAAAAGTTA 3078
Mil.2	TGTTCTTTCTTTTGATATGGATGCAGATGAATCAATATTGATAGCAAAAGGACACAAAAGTTA 3084
Rpi-blb2	TGTTCTTTCTTTTGATATGGATGCAGATGAATCAATACTGATAGCAGAGGACACAAAAGTTA 3114 ****
Mil.1	GAGAACTTGAGAATATTAACGGAACTGTTGATTTCCCTATTCGAAAGATACAAAGAAATATT 3138
Mil.2	GAGAACTTGAGAATATTAGGGGAACTGTTGATTTCCCTATTCGAAAGATACAAATGAATATT 3144
Rpi-blb2	GAGAACTTGACAGCATTAGGGGAACTCGTGCTTTCCCTATTGGAAGATACAGAGGATATT 3174 ***** * ****
Mil.1	TTCAAAAGGTTTCCCAATCTTCAGTTGCTTTTCATTTGAACTCAAGGAGTCATGGGATTAT 3198
Mil.2	TTCAAAAGGTTTCCCAATCTTCAGGTGCTTCAGTTTGAACTCAAGGAGTCATGGGATTAT 3204
Rpi-blb2	TTCAAAAGGCTTCCCAATCTTCAAGTGCTTCATTTCAAACTCAAGGAGTCATGGGATTAT 3234 ***** ****
Mil.1	TCAACAGAGCAACATTGGTTCTCGGAAATTGGATTTCCTAACTGAAC TAGAAACACTCTCT 3258
Mil.2	TCAACAGAGCAACATTGGTTCCCGAAAATTGGATTGCCTAACTGAAC TAGAAACACTCTGT 3264
Rpi-blb2	TCAACAGAGCAATATTGGTTCCCGAAAATTGGATTTCCTAACTGAAC TAGAAACACTCACT 3294 *****
Mil.1	GTAGGTTTAAAGTTCAAAACACAAACGATAGTGGTCCCTCTGTAGCGACAAAATCGGCCG 3318
Mil.2	GTAGGTTTAAAGTTCAAAACACAAACCACTGTGGTCCCTCTGTGTGACAAAATCGGCCG 3324
Rpi-blb2	GTAGATTTTGAAAGATCAAAACACAAATGACAGTGGTCCCTCTGCAGCCATAAAATCGGCCA 3354 ****
Mil.1	TGGGATTTTCACTTCCCTTCAAATTTGAAAATACTGTGTTGCCGTGAATTTCCGCTGACA 3378
Mil.2	TGGGATTTTCACTTCCCTTCAAATTTGAAAGAACTGTGTGTGATGACTTTTCCCTCTGACA 3384
Rpi-blb2	TGGGATTTTCACTTTCCTTCGAGTTTGAAAAGATTGCAATTGCATGAATTTTCCCTCTGACA 3414

	*****	*****	*	*****	*	**	***	***	***	*****	*****	
Mi1.1	TCCGATTCACTATCAACAATAGCGAGACTGCCCAACCTTGAAGAGTTGTCCCTTTATCAT	3438										
Mi1.2	TCCGATTCACTATCAACAATAGCGAGACTGCCCAACCTTGAAGATTTGTCCCTTTATGAT	3444										
Rpi-blb2	TCCGATTCACTATCAACAATAGCGAGACTGCTGAACCTTGAAGAGTTGTACCTTTATCGT	3474										
	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*	
Mi1.1	ACAATCATCCATGGAGAAGAAATGGAACATGGGGAGGAAGACACCTTTGAGAATCTCAAA	3498										
Mi1.2	ACAATCATCCAGGAGAAGAAATGGAACATGGGGAGGAAGACACCTTTGAGAATCTCAAA	3504										
Rpi-blb2	ACAATCATCCATGGGGAAGAAATGGAACATGGGAGAAAGACACCTTTGAGAATCTCAAA	3534										
	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	
Mi1.1	TTTTTGAACTTCAATCAAGTTAGTATTTCCAAGTGGGAGGTTGGAGAGGAATCCTTCCCC	3558										
Mi1.2	TTTTTGAACTTGGCTACTGACTCTTTCCAAGTGGGAGGTTGGAGAGGAATCCTTCCCC	3564										
Rpi-blb2	TGTTTGATGTTGAGTCAAGTGATTCTTTCCAAGTGGGAGGTTGGAGAGGAATCCTTTCCCC	3594										
	*	*****	**	**	*	*	*	*	*	*****	**	***
Mi1.1	AATCTTGAGAAATTAAAACTGCGGGGATGTCAATAAGCTAGAGGAGATTCCACCTAGTTT	3618										
Mi1.2	AATCTTGAGAAATTAAAACTGCAGGAATGTGGTAAGCTTGAGGAGATTCCACCTAGTTT	3624										
Rpi-blb2	ACGCTTGAGAAATTAGAACTGTCTCGACTGTCAATAATCTTGAGGAGATTCCGCTAGTTT	3654										
	*	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
Mi1.1	GGAGATATTTATTCATTGAAATCTATCAAAATTTGTAAAGAGTCCTCAACTTGAAGATTCT	3678										
Mi1.2	GGAGATATTTATTCATTGAAATTTATCAAAATTTGTAAAGAGTCCTCAACTTGAAGATTCT	3684										
Rpi-blb2	GGGATATTTATTCCTTGAAATTTATCGAACTTGTAAAGGAGCCCTCAACTTGAATAATCC	3714										
	**	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
Mi1.1	GCTCTCAAAATTAAGGAATACGCTGAAGATATGAGGGGAGGGACGAGCTTCAGATCCTT	3738										
Mi1.2	GCTCTCAAGATTAAGAAATACGCTGAAGATATGAGAGGAGGGACGATCTTCAGATCCTT	3744										
Rpi-blb2	GCTCTCAAGATTAAGGAATATGCTGAAGATATGAGGGGAGGGACGAGCTTCAGATCCTT	3774										
	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****

Mi1.1	GGCCAAAAGAATATCCCCCTTATTTAAGTAG	3768
Mi1.2	GGCCAGAAGAATATCCCCCTTATTTAAGTAG	3774
Rpi-blb2	GGCCAGAAGGATATCCCGTTATTTAAGTAG	3804
	***** **	*****